

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/645,415

DATE: 06/01/2001

TIME: 12:53:43

Input Set : A:\8002059a.app

Output Set: C:\CRF3\06012001\I645415.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Bermudes, G.
 5 King, I.
 6 Clairmont, C.
 7 Lin, S.
 8 Belcourt, M.

10 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 11 TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
 14 <130> FILE REFERENCE: 8002-059

C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/645,415
 C--> 16 <141> CURRENT FILING DATE: 2000-08-24

16 <150> PRIOR APPLICATION NUMBER: 60/157,581
 17 <151> PRIOR FILING DATE: 1999-10-04
 19 <150> PRIOR APPLICATION NUMBER: 60/157,637
 20 <151> PRIOR FILING DATE: 1999-10-04
 22 <160> NUMBER OF SEQ ID NOS: 61
 24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 26
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Artificial Sequence
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: Forward primer
 34 <400> SEQUENCE: 1
 35 gaagatcttc cggaggagg gaaatg 26
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 44
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial Sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: Reverse primer
 45 <400> SEQUENCE: 2
 46 cgggatccga gctcgagggc ccgggaaagg atctaagaag atcc 44
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 477
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Homo sapiens
 53 <220> FEATURE:
 54 <221> NAME/KEY: CDS
 55 <222> LOCATION: (1)...(474)
 57 <400> SEQUENCE: 3
 58 atg gta cgt agc tcc tct cgc act ccg tcc gat aag ccg gtt gct cat 48
 59 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 60 1 5 10 15
 62 gta gtt gct aac cct cag gca gaa ggt cag ctg cag tgg ctg aac cgt 96
 63 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
 64 20 25 30
 66 cgc gct aac gcc ctg ctg gca aac ggc gtt gag ctc cgt gat aac cag 144

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67 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
68          35          40          45
70 ctc gtg gta cct tct gaa ggt ctg tac ctg atc tat tct caa gta ctg      192
71 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
72          50          55          60
74 ttc aag ggt cag ggc tgc ccg tcg act cat gtt ctg ctg act cac acc      240
75 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
76          65          70          75          80
78 atc agc cgt att gct gta tct tac cag acc aaa gtt aac ctg ctg agc      288
79 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
80          85          90          95
82 gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg      336
83 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
84          100          105          110
86 aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag      384
87 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
88          115          120          125
90 aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat      432
91 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
92          130          135          140
94 ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg      474
95 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
96          145          150          155
98 taa      477
100 <210> SEQ ID NO: 4
101 <211> LENGTH: 158
102 <212> TYPE: PRT
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 4
106 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
107 1          5          10          15
108 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
109          20          25          30
110 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
111          35          40          45
112 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
113          50          55          60
114 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
115          65          70          75          80
116 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
117          85          90          95
118 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
119          100          105          110
120 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
121          115          120          125
122 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
123          130          135          140
124 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
125          145          150          155

```

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127 <210> SEQ ID NO: 5
128 <211> LENGTH: 28
129 <212> TYPE: DNA
130 <213> ORGANISM: Artificial Sequence
132 <220> FEATURE:
133 <223> OTHER INFORMATION: Forward primer
135 <400> SEQUENCE: 5
136   ccgacgcgtt gacacctgaa aactggag                                28
138 <210> SEQ ID NO: 6
139 <211> LENGTH: 29
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Reverse primer
146 <400> SEQUENCE: 6
147   ccgacgcgtg aaaggatctc aagaagatc                                29
149 <210> SEQ ID NO: 7
150 <211> LENGTH: 543
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
154 <220> FEATURE:
155 <223> OTHER INFORMATION: Fusion construct
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (1)...(540)
160 <400> SEQUENCE: 7
161   atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct      48
162   Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
163   1      5      10      15
165   acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc      96
166   Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
167   20      25      30
169   gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag      144
170   Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
171   35      40      45
173   ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt      192
174   Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
175   50      55      60
177   gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg      240
178   Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
179   65      70      75      80
181   atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tcg act cat      288
182   Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
183   85      90      95
185   gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc      336
186   Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
187   100     105     110
189   aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act      384
190   Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
191   115     120     125

```

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```

193   ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt      432
194   Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
195       130                      135                      140
197   ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac      480
198   Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
199   145                      150                      155                      160
201   cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt      528
202   Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
203       165                      170                      175
205   att atc gca ctg taa                      543
206   Ile Ile Ala Leu
207       180

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210 <210> SEQ ID NO: 8

211 <211> LENGTH: 180

212 <212> TYPE: PRT

213 <213> ORGANISM: Artificial Sequence

W--> 215 <220> FEATURE:

W--> 215 <223> OTHER INFORMATION:

215 <400> SEQUENCE: 8

```

216   Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
217       1           5           10           15
218   Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
219       20           25           30
220   Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
221       35           40           45
222   Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
223       50           55           60
224   Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
225       65           70           75           80
226   Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
227       85           90           95
228   Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
229       100          105          110
230   Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
231       115          120          125
232   Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
233       130          135          140
234   Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
235       145          150          155          160
236   Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
237       165          170          175
238   Ile Ile Ala Leu
239       180

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241 <210> SEQ ID NO: 9

242 <211> LENGTH: 801

243 <212> TYPE: DNA

244 <213> ORGANISM: Artificial Sequence

246 <220> FEATURE:

247 <223> OTHER INFORMATION: Fusion construct

→ see item 11 on Euro
Summary
sheet

Please
correct this
error in
subsequent
sequences.

Please Note :

Use f n and/or Xaa have been detected in the Sequence Listing. Please review the Sequenc Listing to ensure that a corresponding explanati n is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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249 <221> NAME/KEY: CDS
250 <222> LOCATION: (1)...(798)
252 <400> SEQUENCE: 9
253 atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct      48
254 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
255 1 5 10 15
257 acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac      96
258 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
259 20 25 30
261 aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt      144
262 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
263 35 40 45
265 tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa      192
266 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
267 50 55 60
269 gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc      240
270 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
271 65 70 75 80
273 tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct      288
274 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
275 85 90 95
277 ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act      336
278 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
279 100 105 110
281 ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat      384
282 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
283 115 120 125
285 gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt      432
286 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
287 130 135 140
289 ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc      480
290 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
291 145 150 155 160
293 atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga      528
294 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
295 165 170 175
297 ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc      576
298 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
299 180 185 190
301 caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg      624
302 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
303 195 200 205
305 aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc      672
306 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
307 210 215 220
309 tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga      720
310 Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
311 225 230 235 240
313 att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa      768

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